IN THE CLAIMS

Claim 1. (Currently amended) A technique for analyzing an output pattern of a biological sample applied to an array to determine the presence of specific constituents within a biological sample applied to the array, wherein the output pattern comprises signals associated with noise, and signals correlating to the biological sample with the signalscorrelating to the biological sample having intensities both greater and less than the signals associated with noise, the method comprising the steps of:

segmenting the output pattern of the array using tessellation;

processing the segmented output pattern usinginterferometry to amplify signals associated with the biological sample, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

determining which signals within the modified output pattern areassociated with specific constituents within the biological sample; and

determining specific constituents within the biological sample based on the signals within the modified output pattern associated with specific constituents within the biological sample.

Claim 2. (Currently amended) A computer code product that determines the presence of specific constituents within an output pattern of a biological sample applied to an array of detectors, wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, the computer code product comprising:

computer code that segments the output pattern using tessellation;

computer code that utilizes interferometric signal processing to amplify signals within the segmented output pattern associated with the biological sample having an intensity lower than the intensity of the signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

computer code that determines which signals within the modified output pattern correlate with specific constituents within the biological sample; and

computer code that determines specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample.

Claim 3. (Currently amended) The computer code product of claim 2 wherein the signal-processingutilizes resonance interferometry to amplify the signals associated with the biological sample.

Claim 4. (Canceled).

Claim 5. (Currently amended) The computer code product of claim 3 wherein the utilized resonance interferometry is either quantum resonance interferometry or stochastic resonance interferometry.

Claims 6-10 (Canceled).

Claim 11. (Previously presented) The method of claim 1, wherein the segmenting step comprises the step of: tessellating the output pattern to match predetermined morphological characteristics.

Claim 12. (Previously presented) The method of claim 1, wherein the tessellation is a fuzzy tessellation.

Claim 13. (Currently amended) The method of claim 1, wherein the segmenting ~~tessellation~~ step uses gradient refocusing.

Claim 14. (Currently amended) The method of claim 1, wherein the segmenting ~~tessellation~~ uses at least one of a Dirichlet tessellation operator or a Delaunay triangulation operator.

Claim 15. (Previously presented) The method of claim 1, wherein the step of processing the output pattern comprises the step of:

generating a resonance pattern by performing a convergent reverberation to yield a resonance pattern representative of resonances between a predetermined set of Quantum Expressor Functions and the tessellated output pattern until a predetermined degree of convergence is achieved between the resonances found in the resonance pattern and expected resonances.

Claim 16. (Previously presented) The method of claim 15 wherein the step of iteratively processing the output pattern by performing a convergent reverberation includes the step of performing a convergent reverberant dynamics resonance analysis of the tessellated output pattern using a resonance stimulus pattern to indicatorsassociated with the constituents within the biological sample represented by the tessellated output pattern.

Claim 17. (Previously presented) The method of claim 16, wherein the step of performing a convergent reverberent dynamics resonance analysis comprises the step of:

determining resonance dynamics relaxation values based upon the processed output pattern and a resonance stimulus.

Claim 18. (Previously presented) The method of claim 17, wherein the step of performing a convergent reverberent dynamics resonance analysis further comprises the step of: filtering the dynamics relaxation values using ensemble boundary and CSR filters to yield a first set of values.

Claim 19. (Previously presented) The method of claim 18, wherein the step of performing a convergent reverberent dynamics resonance analysis further comprises the step of: applying bulk property estimators to the dynamics relaxation values to yield a second set of values.

Claim 20. (Previously presented) The method of claim 19, wherein the step of performing a convergent reverberent dynamics resonance analysis further comprises the steps of:

evaluating the first and second sets of values to determine a degree of resonance convergence; and

determining from the degree of resonance convergence whether a paralysis of dynamics has occurred.

Claim 21. (New) An apparatus for analyzing an output pattern of a biological sample applied to an array to determine the presence of specific constituents within a biological sample applied to the array, wherein the output pattern comprises signals associated with noise, and signals correlating to the biological sample with the signals correlating to the biological sample having intensities both greater and less than the signals associated with noise, the apparatus comprising:

means for segmenting the output pattern of the array using tessellation;

means for processing the segmented output pattern using interferometry to amplify signals associated with the biological sample, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

means for determining which signals within the modified output pattern are associated with specific constituents within the biological sample; and

means for determining specific constituents within the biological sample based on the signals within the modified output pattern associated with specific constituents within the biological sample.

Claim 22. (New) The apparatus of claim 21, wherein the means for segmenting comprises means for tessellating the output pattern to match predetermined morphological characteristics.

Claim 23. (New) The apparatus of claim 21, wherein the tessellation is a fuzzy tessellation.

Claim 24. (New) The apparatus of claim 21, wherein the means for segmenting uses gradient refocusing.

Claim 25. (New) The apparatus of claim 21, wherein the means for segmenting uses at least one of a Dirichlet tessellation operator or a Delaunay triangulation operator.

Claim 26. (New) The apparatus of claim 21, wherein the means for processing comprises means for generating a resonance pattern by performing a convergent reverberation to yield a resonance pattern representative of resonances between a predetermined set of Quantum Expressor Functions and the tessellated output pattern until a predetermined degree of convergence is achieved between the resonances found in the resonance pattern and expected resonances.